# RNA Analysis by Biosynthetic Tagging (RABT): a tool for the identification of cell type-specific RNAs

## Grant Award Details

RNA Analysis by Biosynthetic Tagging (RABT): a tool for the identification of cell type-specific RNAs

**Grant Type:** Tools and Technologies I

**Grant Number:** RT1-01052

**Investigator:**

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| **Name:** | Michael Cleary |
| **Institution:** | University of California, Merced |
| **Type:** | PI |

**Human Stem Cell Use:** Cancer Stem Cell

**Cell Line Generation:** Cancer Stem Cell

**Award Value:** $481,096

**Status:** Closed

## Progress Reports

**Reporting Period:** Year 1

**View Report**

**Reporting Period:** Year 2

**View Report**

**Reporting Period:** NCE

**View Report**

## Grant Application Details

**Application Title:** RNA Analysis by Biosynthetic Tagging (RABT): a tool for the identification of cell type-specific RNAs

**Public Abstract:**

Advancing our understanding of stem cell biology often relies on answers to the following types of questions:

What are the differences in gene expression between a stem cell and the “mature” cell (for example, a neuron or heart cell) made by the stem cell? Answers to such questions can lead to methods for directing stem cells to make specific types of progeny.

How similar are the patterns of gene expression between a “normal” cell and a stem cell-derived cell (for example, a healthy neuron in the brain versus a neuron made from an embryonic stem cell)? Answers to these types of questions can determine exactly how closely a stem cell-derived cell matches the cell it is meant to replace. This information is essential for developing safe and effective therapies.

To best answer these questions, it is necessary to study gene expression in specific cells within their normal setting. This presents a technical hurdle, since the normal setting of a cell is typically within a complex tissue, surrounded by other cell types. To perform these types of experiments using currently available tools, it is necessary to first physically remove cells of interest from all other cells. This type of manipulation can cause unwanted changes in gene expression (giving false results) and is often not technically possible.

I have developed a technique that overcomes this technical hurdle and allows the identification of genes expressed in specific cell types within a mixed population of cells. I propose to develop this technique for the study of stem cells in tissue culture and for the study of stem cells in mice. The tools that are developed as a result of this work will allow previously impossible experiments to be performed and will benefit many areas of stem cell research.

**Statement of Benefit to California:**

Benefits to the development of regenerative medicine therapies in California: The development of the tools described in this proposal will accelerate the progress of regenerative medicine research in California by making previously impossible experiments available to stem cell researchers. The tools described in this proposal are especially well suited for the discovery of novel biomarkers for clinically-relevant cell types, new genetic methods for directing stem cells to generate specific cell types, and new ways to functionally characterize stem cell-derived cell types; three areas of research that CIRM has identified as needing novel technologies.

Benefits to the pharmaceutical and biotechnology industry in California: The types of research that will be made possible using the proposed tools (e.g. the ability to identify cell type specific changes in gene expression in response to drug therapies or in disease states, using whole animal models) will open doors to novel areas of drug discovery, drug development, and diagnostics. Biotechnology and pharmaceutical companies will likely use these tools to launch new research efforts and ultimately new product development. Given the large presence of such industry in California, this will provide benefits to the state’s economy in the form of new jobs, new investment, and increased tax revenue.

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